IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Perry D. Haaland et al.
Serial No.:	10/662,713
Filed:	September 15, 2003
Title:	COMPUTER SOFTWARE AND ALGORITHMS FOR SYSTEMS BIOLOGICALLY LINKED TO CELLULAR PHENOTYPE
Group:	1631
Examiner:	Larry D. RIGGS, II
Confirmation No.:	1008

APPELLANTS' BRIEF

Mail Stop: Appeal Brief
Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

April 20, 2009

Sir:

In response to the Notice of Appeal filed on December 19, 2008, Appellants hereby submit their brief as follows:

Real Party In Interest

The real party in interest is Becton, Dickinson and Company, the assignee of the present application.

Related Appeals and Interferences

There are no other known appeals or interferences that will directly affect or be affected by or have a bearing on the Board's decision in the pending appeal.

Status of Claims

Claims 1-36 have been rejected.

Claims 1-36 are pending. This appeal involves each of these claims.

Status of Amendments

All amendments have been entered. The application was not amended after issuance of the final Office Action mailed August 19, 2008.

Summary of Claimed Subject Matter

Independent claim 1 defines a method for identifying agents that cause a phenotypic change in a cell. Referring to Figs. 1 and 4, for example, a number of receptacles are provided in an array 409. A statistical design that includes generic factor names, factor levels, and experimental runs is subsequently provided. See pg. 15, ln. 6-15 and Figs. 7 and 8. A software program 510 is utilized to generate a computer representation of the statistical design by automatically mapping the identities of agents to the generic factor names, mapping the concentration or amounts of the agents to the factor levels, and mapping the locations of the receptacles within the array to the experimental runs. See pg. 7, ln. 17-26, and Fig. 5. Different mixtures 18 of single agents 20 are placed into select receptacles in the array according to the

computer representation of the statistical design. See pg. 8, ln. 8-12. The mixtures are contacted with the cells 22, and data indicative of a phenotypic change of the contacted cells is acquired. See pg. 8, ln. 17-18. A processor 402, including an algorithm 506 for comparing the phenotypic data with the statistical design, is utilized to identify which mixtures of the single agents or which of the single agents in the mixtures are effective in causing the phenotypic change in the contacted cells 204. See pg. 8, ln. 19-24; pg. 11, ln. 7-10; and pg. 9, ln. 15-18. The statistical design, agent identities, computer representation of the statistical design, acquired data, and results of the algorithm comparison are subsequently stored in one or more databases 500. See pg. 12, ln. 16-18 and pg. 8, ln. 18-27.

Independent claim 32 defines an apparatus for identifying agents that cause a phenotypic change in a cell. As shown in Figs. 4 and 5, the apparatus includes an array of receptacles for receiving different mixtures of agents and fluids that include cells. A statistical design is provided to include generic factor names, factor levels, and experimental runs. See pg. 15, ln. 6-15, and Figs. 7 and 8. A software program 510 generates a computer representation of the statistical design, in part, by mapping the identities of the agents to the generic factor names, mapping the concentration or amounts of the agents to the factor levels, and mapping the locations of the receptacles in the array to the experimental runs. See pg. 7, ln. 17-26. The system also includes a processor 402 including an algorithm 506 for comparing acquired experimental data indicative of phenotypic change in the cells with the statistical design. See pg. 13, ln. 2-11. The processor 402 further identifies which of the agents in the mixtures are effective in causing the phenotypic change in the cells. One or more databases 500 are

also provided for storing the statistical design, the acquired experimental data, and the result of the algorithm comparison. See pg. 12, ln. 16-18.

Ground of Rejection to be Reviewed on Appeal

I. Whether Claims 1-5, 9-12, 15-24, and 32-36 are unpatentable under 35 U.S.C. §102(b) over U.S. Patent No. 6,127,133 to Akong et al. ("Akong").

II. Whether Claims 1 and 6-8 are unpatentable under 35 U.S.C. §103(a) over Akong in view of U.S. Patent No. 5,532,128 to Eggers et al. ("Eggers").

III. Whether Claims 1, 13, and 14 are unpatentable under 35 U.S.C. §103(a) over Akong in view of U.S. Patent No. 6,448,983 to Ali et al. ("Ali").

IV. Whether Claims 1 and 25-29 are unpatentable under 35 U.S.C. §103(a) over Akong in view of Eggers, and further in view of U.S. Patent No. 5,808,918 to Fink et al. ("Fink").

V. Whether Claims 1, 30, and 31 are unpatentable under 35 U.S.C. §103(a) over Akong in view of Eggers, and further in view of Terramani et al. ("Terramani").

Argument

Claims 1-5, 9-12, 15-24, and 32-36 stand rejected under 35 U.S.C. §102(b) as being anticipated by Akong. Claims 1 and 6-8 stand rejected under 35 U.S.C. §103(a) as being obvious over Akong in view of Eggers. Claims 1, 13, and 14 stand rejected under 35 U.S.C. §103(a) as being obvious over Akong in view of Eggers, and further in view of Ali. Claims 1 and 25-29 stand rejected under 35 U.S.C. §103(a) as being obvious over Akong in view of Eggers, and further in view of Fink. Claims 1, 30, and 31 stand rejected under 35 U.S.C. §103(a) as being obvious over Akong in view of Eggers, and further in view of Terramani.

For the reasons set forth below, these rejections should be reversed.

I. Claims 1-5, 9-12, 15-24, and 32-36 are not Anticipated by Akong

The rejection of these claims under 35 U.S.C. §10b(b) is improper, because Akong fails to disclose, or suggest, all of the features recited in these claims.

Independent claim 1

Independent claim 1 defines an automated method is provided for identifying agents that cause a phenotypic change in a cell. The method comprises the steps of:

> providing receptacles in an array;
>
> providing a statistical design including generic factor names, factor levels, and experimental runs;
>
> utilizing a software program to generate a computer representation of said statistical design, said computer representation being generated by automatically mapping the identities of agents to said generic factor names, by mapping the concentration or amounts of said agents to said factor levels, and by mapping the locations of said receptacles within said array to said experimental runs;

placing different mixtures of single said agents into select ones of said receptacles in said array according to said computer representation of said statistical design;

contacting said placed mixtures with said cells;

acquiring data indicative of a phenotypic change in said contacted cells;

utilizing a processor including an algorithm for comparing said phenotypic data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said contacted cells; and

storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired data, and the results of said algorithm comparison in one or more databases.

The method of independent claim 1 provides a number of receptacles and an array, as well as a statistical design that includes generic factor names, factor levels, and experimental runs. A software program is utilized to generate a computer representation of the statistical design by automatically mapping the identities of agents to the generic factor names, mapping the concentration or amounts of the agents to the factor levels, and mapping the locations of the receptacles within the array to the experimental runs. Different mixtures of single agents are placed into select receptacles in the array according to the computer representation of the statistical design. The mixtures are contacted with the cells, and data indicative of a phenotypic change of the contacted cells is acquired. A processor, including an algorithm for comparing the phenotypic data with the statistical design, is utilized to identify which of the mixtures of the single agents or which of the single agents in the mixtures are effective in causing the phenotypic change in the contacted cells. The statistical design,

agent identities, computer representation of the statistical design, acquired data, and results of the algorithm comparison are subsequently stored in one or more databases.

Akong discloses an automated analysis equipment and assay method for studying receptor and ion-channel activity. The apparatus of Akong is intended to automate the process of adding a single reagent to samples and measuring the reaction results in order to minimize lab worker time requirements. As shown in Fig. 5, the device uses a syringe/plunger (135/137) arrangement to draw and pump the reagent from a reagent vessel (145). See col. 6, ln. 58 – col. 7, ln. 4. Accordingly, Akong only automates the process of supplying the same reagent into the assay system. While Akong discloses the use of multiple syringes for dispensing fluids, there is never a discussion of dispensing different agents. See col. 6, ln. 49-51. Consequently, it is not possible to place different mixtures of agents (or reagents) into selected receptacles, as set forth in the claimed invention.

Akong discloses the use of an assay apparatus for measurement in a multi-well plate. The wells are regularly spaced and each well has a specific X,Y location within the rectangular array. See col. 5, ln. 15 – 30. There is no discussion of a statistical design involving, for example, the mapping of different agents. This is to be expected, as Akong utilizes the same agent in all the wells. Akong further discloses that "a test consists of the assay of one or more wells using substantially the same test parameter values," further supporting the use of the same agent. See col. 7, ln. 49 – 51. Akong also discloses a data file which keeps track of the compound/concentration in each well. See Fig. 6 and 7, and corresponding passage. Although various equations are disclosed, they are only useable for calculating the fluorescence signal-to-noise ratio

and intracellular signal-to-noise ratio. See col. 19, ln. 1 – 30. There is clearly no disclosure or suggestion for a statistical design as set forth in the claimed invention.

As previously discussed, only one reagent is used in all the wells during the screening process. The process only measures the phenotype of the cells by determining how they react to one specific agent. See col. 2, ln. 53 – 57. Additionally, Akong merely discusses contacting the cells with a compound. There is no discussion of culturing the cells with multiple, or even one, compounds. Regardless of the manner in which the cells are contacted, however, it is not possible for Akong to obtain data indicative of phenotypic change because the phenotype in Akong's assays does not change. Akong fails to disclose identification of agents that cause a phenotypic change.

Akong indicates that the data from cells treated in the same manner are collected and recorded. In particular, Akong indicates that "results" or "measure values are stored within a microcomputer, which comprises a controller, and later moved to a disk drive for long-term storage." See Fig. 6 and col. 3, ln. 17-20. As previously discussed, Akong does not create a statistical design. Consequently, it is unclear how a statistical design, in part, could be stored in one or more databases. As can be appreciated, a database is vastly different from a simple data file which can easily be represented by a one or two-dimensional array. A database provides relationships between different tables and entries, and can be queried by users to filter and retrieve various information. Merely storing data into a file is certainly not the same as storing (and interrelating) information in a database. Akong provides no disclosure or suggestion for storing a statistical design in a database.

Contrary to Akong, the present invention provides an iterative process that actually solves a problem as opposed to simply collecting test data. See pg. 9, ln. 6 to pg. 10, ln. 26. This can be achieved, for example, by utilizing different agents and/or mixtures of agents and exploring interactions between mixtures of different factors in order to achieve a desired cell fate. Rather than simply measuring the phenotype of the cell, the method of independent claim 1 actually attempts to change the phenotype. See pg. 2, ln. 6-14. Akong simply fails to provide any disclosure for features recited in independent claim 1 such as:

> providing a statistical design including generic factor names, factor levels, and experimental runs;
>
> utilizing a software program to generate a computer representation of said statistical design, said computer representation being generated by automatically mapping the identities of agents to said generic factor names, by mapping the concentration or amounts of said agents to said factor levels, and by mapping the locations of said receptacles within said array to said experimental runs;
>
> placing different mixtures of single said agents into select ones of said receptacles in said array according to said computer representation of said statistical design;
>
> contacting said placed mixtures with said cells;
>
> acquiring data indicative of a phenotypic change in said contacted cells;
>
> utilizing a processor including an algorithm for comparing said phenotypic data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said contacted cells; and
>
> storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired data, and the results of said algorithm comparison in one or more databases.

Accordingly, Akong fails to anticipate independent claim 1.

Dependent Claims 2 – 31

Dependent claims 2-31 stand and fall together with independent claim 1.

Independent claim 32

Independent claim 32 defines a system for identifying agents that cause a phenotypic change in a cell. The system comprises:

> an array of receptacles, selective ones of which are for receiving (i) different mixtures of single said agents, and (ii) fluid including said cells;
>
> a statistical design including generic factor names, factor levels, and experimental runs;
>
> a software program for generating a computer representation of said statistical design, wherein said software program automatically maps the identities of said agents to said generic factor names, maps the concentration of or amounts of said agents to said factor levels, and maps the locations of said receptacles in said array to said experimental runs;
>
> acquired experimental data indicative of said phenotypic change in said cells;
>
> a processor including an algorithm for comparing said experimental data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said cells; and
>
> one or more databases for storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired experimental data, and the results of said algorithm comparison.

According to the system of independent claim 32, an array of receptacles is provided to receive different mixtures of agents and fluids that include cells. A statistical design is provided to include generic factor names, factor levels, and experimental runs. A software program generates a computer representation of the statistical design, in part, by mapping the identities of the agents to the generic factor names, mapping the concentration or amounts of the agents to the factor levels, and mapping the locations

of the receptacles in the array to the experimental runs. The system also includes a processor including an algorithm for comparing acquired experimental data indicative of phenotypic change in the cells with the statistical design. The processor further identifies which of the agents in the mixtures are effective in causing the phenotypic change in the cells. One or more databases are also provided for storing the statistical design, the acquired experimental data, and the result of the algorithm comparison.

As discussed above, Akong fails to provide any disclosure or suggestion for various features of the claimed invention. For example, Akong fails to disclose the use of multiple agents or the creation of a statistical design. In fact, Akong only discloses the use of a single reagent without assay changes. The measured results do not involve a change in the phenotype. Consequently, there can be no disclosure or suggestion for acquiring data indicative of a phenotypic change, or a comparison of the phenotypic data with the statistical design to determine which agent(s) are effective in causing the phenotypic change in the cells. Akong also fails to disclose the use of a database for storing a statistical design. Specifically, Akong fails to disclose or suggest features recited in independent claim 32, such as:

> an array of receptacles, selective ones of which are for receiving (i) different mixtures of single said agents, and (ii) fluid including said cells;
>
> a statistical design including generic factor names, factor levels, and experimental runs;
>
> a software program for generating a computer representation of said statistical design, wherein said software program automatically maps the identities of said agents to said generic factor names, maps the concentration of or amounts of said agents to said factor levels, and maps the locations of said receptacles in said array to said experimental runs;
>
> acquired experimental data indicative of said phenotypic change in said cells;

a processor including an algorithm for comparing said experimental data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said cells; and

one or more databases for storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired experimental data, and the results of said algorithm comparison.

Accordingly, Akong fails to anticipate independent claim 32.

Dependent Claims 33 – 36

Dependent claims 33-36 stand and fall together with independent claim 32.

II. Claims 1 and 6-8 are not Obvious over Akong in view of Eggers

The rejection of Claims 1 and 6-8 is improper with respect to independent claim 1, inasmuch as it suggests that all the features of independent claim 1 are not disclosed by Akong. The Examiner purports to support this rejection by indicating that Eggers is only relied upon for disclosing the features of dependent claims 6-8, and that independent claim 1 is not rejected under 35 USC §103(a). See pg. 14, ln. 14-20 of the final Office Action mailed August 19, 2008.

Regardless of the Examiner's position, the Office Action plainly recites "Claims 1 and 6-8 are rejected under 35 U.S.C. 103(a) as being unpatentable over Akong et al. (US 6,127,133) in view of Eggers et al. (US 5,532,128)." See pg. 9, ln. 5-7 of the final Office Action mailed August 19, 2008. Claim 1 is clearly part of the rejection. Although Applicants clearly identified this inconsistency in the prior Amendment, nothing was

done and the rejection was repeated in the final Office Action without correction. See page 21 of Amendment filed March 28, 2008.

If the Examiner's position is that claims 1 and 6-8 are rejected under 35 U.S.C. §103(a), as set forth on page 9 of the Office Action, then Applicants respectfully submit that the rejection is improper and/or supports the lack of anticipation of independent claim 1 by Akong. Alternatively, if the Examiner's position is that claim 1 is not rejected under 35 U.S.C. §103(a), as set forth on page 14, then Applicants respectfully submit that the Office Action is defective. In any event, independent claim 1 is not anticipated by Akong, for the reasons set forth above.

III. Claims 1, 13, and 14 are not Obvious over Akong in view of Eggers and Ali

The rejection of Claims 1, 13, and 14 is improper with respect to independent claim 1, inasmuch as it suggests that all the features of independent claim 1 are not disclosed by Akong. The Examiner purports to support this rejection by indicating that Eggers and Ali are only relied upon for disclosing the features of dependent claims 13 and 14, and that independent claim 1 is not rejected under 35 USC §103(a). See pg. 14, ln. 14-20 of the final Office Action mailed August 19, 2008.

Regardless of the Examiner's position, the Office Action plainly recites "Claims 1 and 6-8 are rejected under 35 U.S.C. 103(a) as being unpatentable over Akong et al. in view of Eggers et al. as applied to claims 1 and 6-8 above, and further in view of Ali et al. (US 5,532,128)." See pg. 11, ln. 3-5 of the final Office Action mailed August 19, 2008. Claim 1 is clearly part of the rejection. Although Applicants clearly identified this

inconsistency in the prior Amendment, nothing was done and the rejection was repeated in the final Office Action without correction. See page 21 of Amendment filed March 28, 2008.

If the Examiner's position is that claims 1, 13, and 14 are rejected under 35 U.S.C. §103(a), as set forth on page 11 of the Office Action, then Applicants respectfully submit that the rejection is improper and/or supports the lack of anticipation of independent claim 1 by Akong. Alternatively, if the Examiner's position is that claim 1 is not rejected under 35 U.S.C. §103(a), as set forth on page 14, then Applicants respectfully submit that the Office Action is defective. In any event, independent claim 1 is not anticipated by Akong, for the reasons set forth above.

IV. Claims 1 and 25-29 are not Obvious over Akong in view of Eggers and Fink

The rejection of Claims 1 and 25-29 is improper with respect to independent claim 1, inasmuch as it suggests that all the features of independent claim 1 are not disclosed by Akong. The Examiner purports to support this rejection by indicating that Eggers and Fink are only relied upon for disclosing the features of dependent claims 25-29, and that independent claim 1 is not rejected under 35 USC §103(a). See pg. 14, ln. 14-20 of the final Office Action mailed August 19, 2008.

However, the Office Action plainly recites "Claims 1 and 25-29 are rejected under 35 U.S.C. 103(a) as being unpatentable over Akong et al. in view of Eggers et al. as applied to claims 1 and 6-8 above, and further in view of Fink et al. (US 5,808,918)." See pg. 11, ln. 15-17 of the final Office Action mailed August 19, 2008. Claim 1 is

clearly part of the rejection. Although Applicants clearly identified this inconsistency in the prior Amendment, nothing was done and the rejection was repeated in the final Office Action without correction. See page 21 of Amendment filed March 28, 2008.

If the Examiner's position is that claims 1 and 25-27 are rejected under 35 U.S.C. §103(a), as set forth on page 11 of the Office Action, then Applicants respectfully submit that the rejection is improper and/or supports the lack of anticipation of independent claim 1 by Akong. Alternatively, if the Examiner's position is that claim 1 is not rejected under 35 U.S.C. §103(a), as set forth on page 14, then Applicants respectfully submit that the Office Action is defective. In any event, independent claim 1 is not anticipated by Akong, for the reasons set forth above.

V, Claims 1, 30, and 31 are not obvious over Akong in view of Eggers and Terramani

The rejection of Claims 1, 30, and 31 is improper with respect to independent claim 1, inasmuch as it suggests that all the features of independent claim 1 are not disclosed by Akong. The Examiner purports to support this rejection by indicating that Eggers and Terramani are only relied upon for disclosing the features of dependent claims 30 and 31, and that independent claim 1 is not rejected under 35 USC §103(a). See pg. 14, ln. 14-20 of the final Office Action mailed August 19, 2008.

The Office Action, however, plainly recites "Claims 1, 30, and 31 are rejected under 35 U.S.C. 103(a) as being unpatentable over Akong et al. in view of Eggers et al. as applied to claims 1 and 6-8 above, and further in view of Terramani, et al. *In Vitro Cell. Dev. Biol.; Human Macrovascular Endothelial Cells: Optimization of Culture*

Conditions, 2000, 36, 125-132." See pg. 12, ln. 15-19 of the final Office Action mailed August 19, 2008. Claim 1 is clearly part of the rejection. Although Applicants clearly identified this inconsistency in the prior Amendment, nothing was done and the rejection was repeated in the final Office Action without correction. See page 21 of Amendment filed March 28, 2008.

If the Examiner's position is that claims 1, 30, and 31 are rejected under 35 U.S.C. §103(a), as set forth on page 12 of the Office Action, then Applicants respectfully submit that the rejection is improper and/or supports the lack of anticipation of independent claim 1 in view of Akong. Alternatively, if the Examiner's position is that claim 1 is not rejected under 35 U.S.C. §103(a), as set forth on page 14, then Applicants respectfully submit that the Office Action is defective. In any event, independent claim 1 is not anticipated by Akong, for the reasons set forth above.

CONCLUSION

For the foregoing reasons, the final rejection of the claims should be reversed.

FEES

The Appeal Brief fee is submitted herewith.

AUTHORIZATION

Applicants request any shortage or excess in fees in connection with the filing of this paper, including extension of time fees, and for which no other form of payment is offered, be charged or credited to Becton, Dickinson and Company (ATSK), Account No. 06-4154 (Case No. P-5768(1385.45509X00)).

Respectfully submitted,
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CLAIMS APPENDIX

1. An automated method for identifying agents that cause a phenotypic change in a cell comprising the steps of:

providing receptacles in an array;

providing a statistical design including generic factor names, factor levels, and experimental runs;

utilizing a software program to generate a computer representation of said statistical design, said computer representation being generated by automatically mapping the identities of agents to said generic factor names, by mapping the concentration or amounts of said agents to said factor levels, and by mapping the locations of said receptacles within said array to said experimental runs;

placing different mixtures of single said agents into select ones of said receptacles in said array according to said computer representation of said statistical design;

contacting said placed mixtures with said cells;

acquiring data indicative of a phenotypic change in said contacted cells;

utilizing a processor including an algorithm for comparing said phenotypic data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said contacted cells; and

storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired data, and the results of said algorithm comparison in one or more databases.

2. The method of claim 1, wherein a user inputs said identities and said concentrations or amounts of said agents into said software program.

3. The method of claim 1, wherein a user inputs said statistical design into said software program.

4. The method of claim 1, further comprising the step of generating a computer program for a robotic system to perform said placing step.

5. The method of claim 1, further comprising the step of placing single said agents into others of said receptacles in said array.

6. The method of claim 1, wherein said receptacles includes a surface which is coated with an agent-immobilizing material.

7. The method of claim 6, further comprising the step of covalently immobilizing said mixtures of single agents to said agent-immobilizing material on said receptacle surface.

8. The method of claim 6, wherein said agent-immobilizing material is a biocompatible polymer that includes reactive groups for covalently immobilizing said agents.

9. The method of claim 1, wherein the all of said databases are a single integrated or federated database.

10. The method of claim 1, wherein the identification of said mixtures that are effective in causing said phenotypic change is determined by fitting statistical models

11. The method of claim 1, wherein the identification of said mixtures that are effective in causing said phenotypic change is determined by direct comparisons among said mixtures and/or against controls.

12. The method of claim 1, wherein said processor further includes an algorithm for comparing the performance of said single agents or said mixtures of said single agents over multiple experiments in order determine trends or patterns, wherein said comparisons are stored in a database and can be periodically updated.

13. The method of claim 1, wherein said statistical design is a fractional factorial design, a d-optimal design, a mixture design, or a Plackett-Burman design.

14. The method of claim 1, wherein said statistical design is a space-filling design based a coverage criteria, a lattice design, or a latin square design.

15. The method of claim 1, wherein said agents comprise cellular ligands and/or extrinsic factors.

16. The method of claim 15, wherein said agents are selected from the group consisting of extracellular matrix proteins, extracellular matrix protein fragments, peptides, growth factors, cytokines and combinations thereof.

17. The method of claim 1, further comprising repeating said steps with a subset of said identified mixture of single agents.

18. The method of claim 1, further comprising repeating said steps, wherein the concentrations of single agents in said identified mixture of single agents are varied.

19. The method of claim 1, further comprising the step of identifying internal cellular mechanisms associated with said phenotypic change.

20. The method of claim 19, wherein said identifying of cellular mechanisms comprises extracting scientific information on cellular pathways and comparing said extracted information with said identified mixture of single agents and said phenotypic change.

21. The method of claim 20, wherein said information is computer-extracted.

22. The method of claim 20, wherein said information comprises gene expression data, protein expression data, cellular phenotype data, signal transduction data, data on cellular pathways, and combinations thereof.

23. The method of claim 19, wherein said identifying of cellular mechanisms comprises identifying genes and/or proteins expressed by said cells in the presence of said identified mixture of single agents.

24. The method of claim 19, wherein said identifying of cellular mechanisms comprises identifying which receptors on said cells are activated in the presence of said identified mixture of single agents.

25. The method of claim 1, wherein said processor further includes a first application program for calculating the likelihood that a cellular pathway, protein, or gene is involved in changes in cellular phenotype associated with said identified mixture of single agents, wherein said cellular pathway or protein is determined using scientific information.

26. The method of claim 25, wherein said scientific information is selected from the group consisting of gene expression data, protein expression data, cellular phenotype data, signal transduction data, data on cellular pathways, and combinations thereof.

27. The method of claim 25, wherein said scientific information is stored in one or more databases.

28. The method of claim 25, wherein said scientific information comprises the identification of genes and/or proteins expressed by said cells in the presence of said identified mixture of single agents.

29. The method of claim 25, wherein said scientific information comprises the identification of receptors on said cells which are activated in the presence of said identified mixture of single agents.

30. The method of claim 1, wherein said phenotypic data is acquired by immunocytochemistry analysis.

31. The method of claim 30, wherein said immunocytochemistry analysis determines whether biological markers are present that indicate proliferation and/or differentiation of said cells in the presence of a particular mixture of single agents.

32. A system for identifying agents that cause a phenotypic change in a cell, comprising:

an array of receptacles, selective ones of which are for receiving (i) different mixtures of single said agents, and (ii) fluid including said cells;

a statistical design including generic factor names, factor levels, and experimental runs;

a software program for generating a computer representation of said statistical design, wherein said software program automatically maps the identities of said agents to said generic factor names, maps the concentration of or amounts of said agents to said factor levels, and maps the locations of said receptacles in said array to said experimental runs;

acquired experimental data indicative of said phenotypic change in said cells;

a processor including an algorithm for comparing said experimental data with said statistical design to identify which of said mixtures of single agents and/or which of said single agents in said mixtures are effective in causing said phenotypic change in said cells; and

one or more databases for storing said statistical design, said agent identities, said computer representation of said statistical design, said acquired experimental data, and the results of said algorithm comparison.

33. The system of claim 32, wherein said databases are a single integrated or federated database.

34. The system of claim 32, further comprising a robotic system to place said mixtures of single agents correctly in said receptacles based on said computer representation of said statistical design.

35. The system of claim 34, further comprising a computer program with instructions for said robotic system to place said mixtures of single agents correctly in said receptacles based on said computer representation of said statistical design.

36. The system of claim 32, wherein said processor further includes an algorithm for comparing the performance of said single agents or said mixtures of said single agents over multiple experiments in order to determine trends or patterns, wherein said comparisons are stored in a database.

EVIDENCE APPENDIX

None

RELATED PROCEEDINGS APPENDIX

None